

SEQUENCE LISTING

SEQ ID NO: 1
Sequence Length: 1013
Sequence Type: Nucleic acid
Stranded nos: Single
Topology: Linear
Molecular Type: cDNA

Sub B7

GAATTCGGCA CGAGGATCT GG ATG GCA TCT ACT TCG TAT GAC TAT TGC AGA	49
Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg	
5 10	
GTG CCC ATG GAA GAC GGG GAT AAG CGC TGT AAG CTT CTG CTG GGG ATA	97
Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile	
15 20 25	
GGA ATT CTG GTG CTC CTG ATC ATC GTG ATT CTG GGG GTG CCC TTG ATT	145
Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile	
30 35 40	
ATC TTC ACC ATC AAG GCC AAC AGC GAG GCC TGC CGG GAC GGC CTT CGG	193
Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg	
45 50 55	
GCA GTG ATG GAG TGT CGC AAT GTC ACC CAT CTC CTG CAA CAA GAG CTG	241
Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu	
60 65 70	
ACC GAG GCC CAG AAG GGC TTT CAG GAT GTG GAG GCC CAG GCC GCC ACC	289
Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr	
75 80 85 90	
TGC AAC CAC ACT GTG ATG GCC CTA ATG GGT TCC CTG GAT GCA GAG AAG	337
Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys	
95 100 105	
GCC CAA GGA CAA AAG AAA GTG GAG GAG CTT GAG GGA GAG ATC ACT ACA	385
Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr	
110 115 120	
TTA AAC CAT AAG CTT CAG GAC GCG TCT GCA GAG GTG GAG CGA CTG AGA	433
Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg	
125 130 135	
AGA GAA AAC CAG GTC TTA AGC GTG AGA ATC GCG GAC AAG AAG TAC TAC	481
Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr	
140 145 150	
CCC AGC TCC CAG GAC TCC AGC TCC GCT GCG GCG CCC CAG CTG CTG ATT	529
Pro Ser Ser Gln Asp Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile	
155 160 165 170	
GTG CTG CTG GGC CTC AGC GCT CTG CTG CAG TGA GATCCCAGGA AGCTGGCACA	582
Val Leu Leu Gly Leu Ser Ala Leu Leu Gln ***	
175 180 185	
TCTTGAAGG TCCGTCCTGC TCGGCTTTTC GCTTGAACAT TCCCTTGATC TCATCAGTTC	642
TGAGCGGGTC ATGGGGCAAC ACGGTTAGCG GGGAGAGCAC GGGGTAGCCG GAGAAGGGCC	702
TCTGGAGCAG GTCTGGAGGG GCCATGGGGC AGTCCTGGGT GTGGGGACAC AGTCGGGTTG	762
ACCCAGGGCT GTCTCCCTCC AGAGCCTCCC TCCGACAAT GAGTCCCCC TCTTGTCTCC	822
CACCTGAGA TTGGGCATGG GGTGCGGTGT GGGGGCATG TGCTGCCTGT TGTATGGGT	882
TTTTTTTTCG GGGGGGGTTG CTTTTTTCTG GGGTCTTTGA GCTCCAAAAA AATAAACACT	942
TCCTTTGAGG GAGAGCACCA CACCTTAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAATTC	1002
GGGCGGCCGC C	1013

SEQ ID NO: 2
Sequence Length: 379
Sequence Type: Nucleic acid
Topology: Linear
Molecular Type: cDNA
Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCT AGT CAG GAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val	
15 20 25	
AAT ACT GCT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40 45	
CTG CTG ATC TAC TCG GCA TCC AAC CGG TAC ACT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg	
50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCT ACC TAC TAC TGC CAG CAA CAT TAT AGT	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser	
80 85 90	
ACT CCA TTC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 3
Sequence Length: 418
Sequence Type: Nucleic acid
Topology: Linear
Molecular Type: cDNA
Sequence

ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT	48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	
-15 -10 -5	
GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
CCT GGG GCC TCA GTG AAG GTT TCC TGC AAG GCA TCT GGA TAC ACC TTC	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	

ACT	CCC	TAC	TGG	ATG	CAG	TGG	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GGG	CTT	192
Thr	Pro	Tyr	Trp	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
30					35					40					45	
GAG	TGG	ATG	GGA	TCT	ATT	TTT	CCT	GGA	GAT	GGT	GAT	ACT	AGG	TAC	AGT	240
Glu	Trp	Met	Gly	Ser	Ile	Phe	Pro	Gly	Asp	Gly	Asp	Thr	Arg	Tyr	Ser	
				50					55					60		
CAG	AAG	TTC	AAG	GGC	AGA	GTC	ACC	ATG	ACC	GCA	GAC	AAG	TCC	ACG	AGC	288
Gln	Lys	Phe	Lys	Gly	Arg	Val	Thr	Met	Thr	Ala	Asp	Lys	Ser	Thr	Ser	
			65				70						75			
ACA	GCC	TAC	ATG	GAG	CTG	AGC	AGC	CTG	AGA	TCT	GAG	GAC	ACG	GCC	GTG	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
		80				85					90					
TAT	TAC	TGT	GCG	AGA	GGA	TTA	CGA	CGA	GGG	GGG	TAC	TAC	TTT	GAC	TAC	384
Tyr	Tyr	Cys	Ala	Arg	Gly	Leu	Arg	Arg	Gly	Gly	Tyr	Tyr	Phe	Asp	Tyr	
	95					100					105					
TGG	GGG	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	G					418
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
110					115					120						

SEQ ID NO: 4

Sequence Length: 418

Sequence Type: Nucleic acid

Topology: Linear

Molecular Type: cDNA

Sequence

ATG	GAC	TGG	ACC	TGG	AGG	GTC	TTC	TTC	TTG	CTG	GCT	GTA	GCT	CCA	GGT	48
Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Phe	Leu	Leu	Ala	Val	Ala	Pro	Gly	
				-15					-10					-5		
GCT	CAC	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCT	GAG	GTG	AAG	AAG	96
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
		-1	1				5					10				
CCT	GGG	GCC	TCA	GTG	AAG	GTT	TCC	TGC	AAG	GCA	TCT	GGA	TAC	ACC	TTC	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15				20					25						
ACT	CCC	TAC	TGG	ATG	CAG	TGG	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GGG	CTT	192
Thr	Pro	Tyr	Trp	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	30				35					40					45	
GAG	TGG	ATG	GGA	TCT	ATT	TTT	CCT	GGA	GAT	GGT	GAT	ACT	AGG	TAC	AGT	240
Glu	Trp	Met	Gly	Ser	Ile	Phe	Pro	Gly	Asp	Gly	Asp	Thr	Arg	Tyr	Ser	
				50					55					60		
CAG	AAG	TTC	AAG	GGC	AGA	GTC	ACC	ATC	ACC	GCA	GAC	AAG	TCC	ACG	AGC	288
Gln	Lys	Phe	Lys	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	
			65				70						75			
ACA	GCC	TAC	ATG	GAG	CTG	AGC	AGC	CTG	AGA	TCT	GAG	GAC	ACG	GCC	GTG	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
		80				85					90					
TAT	TAC	TGT	GCG	AGA	GGA	TTA	CGA	CGA	GGG	GGG	TAC	TAC	TTT	GAC	TAC	384
Tyr	Tyr	Cys	Ala	Arg	Gly	Leu	Arg	Arg	Gly	Gly	Tyr	Tyr	Phe	Asp	Tyr	
	95					100					105					
TGG	GGG	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	G					418
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser						
110					115					120						